200205

From: Ramirez, Delia
Sent: Wednesday, August 30, 2006 12:57 PM
To: STIC-Biotech/ChemLib
Subject: 10/824581

Hi,

I would like to request an alignment of SEQ ID NO:2 and 4.

Please provide a printout of the results.

Thank you very much,

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********************
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____
```

```
********************
        Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___
```

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******************
Vendors and cost where applicable
   STN:_____
   DIALOG:_____
   QUESTEL/ORBIT:_____
   LEXIS/NEXIS:_____
   SEQUENCE SYSTEM:_____
   WWW/Internet:_____
   Other (Specify):_____
```

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              GenCore version 5.1.9
         Copyright (c) 1993 - 2006 Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:       September  6, 2006, 10:56:15 ; Search time 0.001 Seconds
                                            (without alignments)
                                           28.014 Million cell updates/sec

Title:
Perfect score:   us-10-824-581-2
Sequence:        955
             1 MTKTFKTLDDFLGTHFIYTY.........YKEMPNDIRNGKYLIKTTIV 174

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1 seqs, 161 residues

Total number of hits satisfying chosen parameters:        1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       us-10-824-581-4:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                      %
Result        Query
No.   Score   Match Length DB  ID                          Description
----- -----   ----- ------ -- -------                      -----------
  1   666.5    69.8    161  1   us-10-824-581-4


                             ALIGNMENTS

RESULT 1
us-10-824-581-4
Query Match            69.8%;   Score 666.5;  DB 1;  Length 161;
Best Local Similarity  71.9%;   Pred. No. 0;
Matches  115;  Conservative  26;  Mismatches  18;  Indels  1;  Gaps     1;

Qy     8 LDDFLGTHFIYTYDNGWEYEWYAKNDHTVDYRIHGGMVAGRWVTDQKADIVMLTEGIYKI 67
           ::::|:|::|| |||||| ||||| |::||||||| |||||||| |::||  ||||:||:.
Db     1 MENFIGSHMIYTYENGWEYEIYIKNDHTIDYRIHSGMVAGRWVRDQEVNIVKLTEGVYKV 60

Qy    68 SWTEPTGTDVALDFMPNEKKLHGTIFFPKWVEEHPEITVTYQNEHIDLMEQSREKYATYP 127
          |||||||||| ||:|:|||:::|||||| | ||:|||||||||||:|||||::||||||| |||
Db    61 SWTEPTGTDVSLNFMPNEKRMHGIIFFPKWVHEHPEITVCYQNDHIDLMKESREKYETYP 120

Qy   128 KLVVPEFANITYM-GEGQNNEDVISEAPYKEMPNDIRNGK 166
          ||:|||||  |:| :|:|:|:||  :.||::||:
Db   121 KYVVPEFAEITFLKNEGVDNEEVISKAPVEGMTDDIRAGR 160


Search completed: September  6, 2006, 10:56:15
Job time : 0.001 secs
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